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Show:

☐ 1: [NM\\_006044](#). Homo sapiens hist...[gi:13128863]

Links

LOCUS NM\_006044 4099 bp mRNA linear PRI 04-OCT-2003

DEFINITION Homo sapiens histone deacetylase 6 (HDAC6), mRNA.

ACCESSION NM\_006044

VERSION NM\_006044.2 GI:13128863

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4099)

AUTHORS Hook,S.S., Orian,A., Cowley,S.M. and Eisenman,R.N.

TITLE Histone deacetylase 6 binds polyubiquitin through its zinc finger (PAZ domain) and copurifies with deubiquitinating enzymes

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (21), 13425-13430 (2002)

MEDLINE 22269913

PUBMED 12354939

REMARK GeneRIF: the C terminus of HDAC 6 is both necessary and sufficient for specific association with polyubiquitin

REFERENCE 2 (bases 1 to 4099)

AUTHORS Mahlknecht,U., Schnittger,S., Landgraf,F., Schoch,C., Ottmann,O.G., Hiddemann,W. and Hoelzer,D.

TITLE Assignment of the human histone deacetylase 6 gene (HDAC6) to X chromosome p11.23 by in situ hybridization

JOURNAL Cytogenet. Cell Genet. 93 (1-2), 135-136 (2001)

MEDLINE 21367618

PUBMED 11474198

REFERENCE 3 (bases 1 to 4099)

AUTHORS Grozinger,C.M., Hassig,C.A. and Schreiber,S.L.

TITLE Three proteins define a class of human histone deacetylases related to yeast Hda1p

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (9), 4868-4873 (1999)

MEDLINE 99238449

PUBMED 10220385

REFERENCE 4 (bases 1 to 4099)

AUTHORS Pazin,M.J. and Kadonaga,J.T.

TITLE What's up and down with histone deacetylation and transcription?

JOURNAL Cell 89 (3), 325-328 (1997)

MEDLINE 97294375

PUBMED 9150131

REFERENCE 5 (bases 1 to 4099)

AUTHORS Wolffe,A.P.

TITLE Transcriptional control. Sinful repression

JOURNAL Nature 387 (6628), 16-17 (1997)

MEDLINE 97284401

PUBMED 9139815

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from [AJ011972.1](#).



On Feb 26, 2001 this sequence version replaced gi:5174488.

Summary: Histones play a critical role in transcriptional regulation, cell cycle progression, and developmental events. Histone acetylation/deacetylation alters chromosome structure and affects transcription factor access to DNA. The protein encoded by this gene belongs to class II of the histone deacetylase/acuc/apha family. It contains an internal duplication of two catalytic domains which appear to function independently of each other. This protein possesses histone deacetylase activity and represses transcription.

COMPLETENESS: complete on the 3' end.

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//

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Oct 28 2003 13:06:52



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

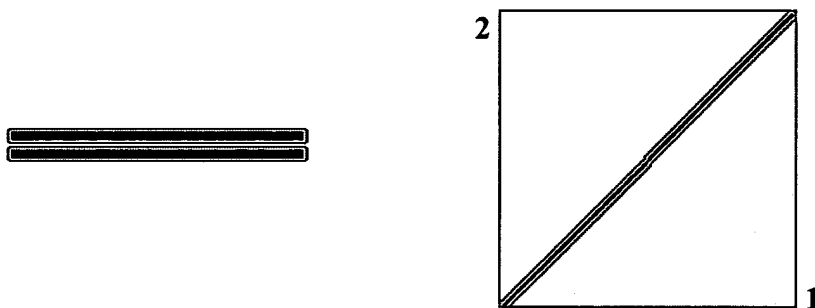
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.1.2 [Oct-19-2000]

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**Sequence 2** gi 13128863 Homo sapiens histone deacetylase 6 (HDAC6), mRNA **Length** 4099 (1 .. 4099)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 7849 bits (4082), Expect = 0.0

Identities = 4098/4099 (99%)

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 Sbjet: 3721 gatatgccccacccacactaagccccagaatacgggtccctcttcaccttctgaggcc  
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Sbjct:          4021 tcatgaggataacattggcgggaggggagttaactggcaggcatggcaaggttgcatt

Query:          4081 taataaagtacaagctggt 4099
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Sbjct:          4081 taataaagtacaagctggt 4099

```

CPU time: 0.21 user secs. 0.09 sys. secs 0.30 total secs.

Gapped  
 Lambda K H  
 1.33 0.621 1.12

Gapped  
 Lambda K H  
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Hits to DB: 37  
 Number of Sequences: 0  
 Number of extensions: 37  
 Number of successful extensions: 25  
 Number of sequences better than 10.0: 1  
 length of query: 4099  
 length of database: 4,430,590,239  
 effective HSP length: 26  
 effective length of query: 4073  
 effective length of database: 4,429,730,003  
 effective search space: 18042290302219  
 effective search space used: 18042290302219  
 T: 0  
 A: 0  
 X1: 6 (11.5 bits)  
 X2: 26 (50.0 bits)  
 S1: 12 (23.8 bits)  
 S2: 21 (41.1 bits)